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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 23:36:27 ; Search time 5307.2 Seconds (without alignments)
 2005.538 Million cell updates/sec

Title: US-09-719-748-1_COPY_98_886
 Perfect score: 789

Sequence: 1 tatgacatcgagggagct.....cttcagacacccgtgatc 789

scoring table: IDENTITY_NUC
 Gapext 1.0

Searched: 13736207 seqs, 674847742 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_lespl:*

7: em_esrro:*

8: em_htcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htcc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_phn:*

16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	562.8	71.3	1729	AK004550
2	541.4	68.6	882	AJ322362
3	501.4	63.5	830	BG868701
4	494.6	62.7	976	BC012210
5	483	61.2	972	BI554559
6	464.2	58.8	1199	AK009701
7	459.2	58.8	869	W82115
8	428.2	54.3	671	BF727181
9	425.6	53.9	982	BF976537
10	422.2	53.9	585	BG384579
11	414	52.5	708	AW76323
12	413	52.3	649	B1046467
13	411.4	52.1	1127	BE733355
14	410.6	52.0	555	BF087508
15	409	51.8	1058	BF421064
16	408.2	51.7	663	BF019508
17	403.4	51.1	565	BF075625

JOURNAL COMMENT		Unpublished (1996)
Contact: Marra M/Mouse EST Project		
WASHU-HMMI Mouse EST Project		
Washington University School of Medicine		
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: mouseest@ewton.wustl.edu		
This clone is available royalty-free through LNL; contact the		
IMAGE Consortium (info@image.llnl.gov) for further information.		
MGI:247370		
This read is a RESEQUENCE of a previously sequenced mouse clone		
This read has been verified (found to hit its original self in the		
correct orientation)		
Seq primer: -40RP from Gibco		
High quality sequence stop: 442.		
Location/Qualifiers		
1. . 882		
/organism="Mus musculus"		
/db_xref="taxon:10090"		
/clone_id="Soares mouse pJNMF19.5"		
/dev_stage="19.5 dpc total fetus"		
/lab_host="DH10B (ampicillin resistant)"		
/note="Vector: pRT3D (Pharmacia) with a modified		
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA		
was primed with a Not I - oligo(dt) primer [5',		
TGTACCACTCTGAGCTGGGACGGCCATTTTTTTTT 3'],		
double-stranded cDNA was size selected, ligated to Eco RI		
adapters (Pharmacia), digested with Not I and cloned into		
the Not I and Eco RI sites of a modified pRT3 vector		
(Pharmacia). Library went through one round of		
normalization to a Cot = 5. Library constructed by Bento		
Soares and M. Farina Bonaldo. RNA was kindly provided by		
Dr. Minoru Ko (Wayne State University)."		
BASE COUNT	246	a 210 c 227 g 193 t 6 others
ORIGIN		
FEATURES		
source		
Query Match	68.6%	Score 541.4; DB 9; Length 882;
Best Local Similarity	89.8%	Pred. No. 3.1e-120; Mismatches 0; Indels 1; Gaps 1;
Matches	589;	Conservative 0; Mismatches 66; Indels 1; Gaps 1;
LOCUS	BG868701	LOCUS BG868701 NCL_CGAP SG2
DEFINITION	60278752F1	60278752F1 Mus musculus cDNA clone IMAGE:4913788
ACCESSION	60278752F1	5', mRNA sequence.
VERSION	BG868701	EST.
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
TITLE	NIH-MGC http://mgc.ncbi.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished	
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: rgs@MAIL.nih.gov	
	Tissue Procurement: Jeffrey E. Green, M.D.	
	cDNA Library Preparation: Life Technologies, Inc.	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Plate: ILM10819 row: k column: 05	
FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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DEFINITION	60278752F2	5', mRNA sequence.
ACCESSION	60278752F2	EST.
VERSION	BG868702	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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	Plate: ILM10819 row: k column: 05	
FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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DEFINITION	60278752F3	5', mRNA sequence.
ACCESSION	60278752F3	EST.
VERSION	BG868703	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
TITLE	NIH-MGC http://mgc.ncbi.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)
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	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Plate: ILM10819 row: k column: 05	
FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
LOCUS	BG868704	LOCUS BG868704 NCL_CGAP SG2
DEFINITION	60278752F4	5', mRNA sequence.
ACCESSION	60278752F4	EST.
VERSION	BG868704	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
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	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
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Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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DEFINITION	60278752F5	5', mRNA sequence.
ACCESSION	60278752F5	EST.
VERSION	BG868705	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
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	DNA Sequencing by: Incyte Genomics, Inc.	
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Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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DEFINITION	60278752F6	5', mRNA sequence.
ACCESSION	60278752F6	EST.
VERSION	BG868706	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
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	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
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Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
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ACCESSION	60278752F7	EST.
VERSION	BG868707	
KEYWORDS		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
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FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
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ACCESSION	60278752F8	EST.
VERSION	BG868708	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Plate: ILM10819 row: k column: 05	
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Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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ACCESSION	60278752F9	EST.
VERSION	BG868709	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
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ACCESSION	60278752F10	EST.
VERSION	BG868710	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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JOURNAL	Unpublished	
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	DNA Sequencing by: Incyte Genomics, Inc.	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov	
	Plate: ILM10819 row: k column: 05	
FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
LOCUS	BG868711	LOCUS BG868711 NCL_CGAP SG2
DEFINITION	60278752F11	5', mRNA sequence.
ACCESSION	60278752F11	EST.
VERSION	BG868711	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 830)	
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JOURNAL	Unpublished	
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FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
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ACCESSION	60278752F12	EST.
VERSION	BG868712	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
LOCUS	BG868713	LOCUS BG868713 NCL_CGAP SG2
DEFINITION	60278752F13	5', mRNA sequence.
ACCESSION	60278752F13	EST.
VERSION	BG868713	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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	Plate: ILM10819 row: k column: 05	
FEATURES		
source		
Query Match	63.5%	Score 501.4; DB 10; Length 830;
Best Local Similarity	90.5%	Pred. No. 1.4e-110; Mismatches 0; Indels 5; Gaps 5;
Matches	590;	Conservative 0; Mismatches 57; Indels 5; Gaps 5;
LOCUS	BG868714	LOCUS BG868714 NCL_CGAP SG2
DEFINITION	60278752F14	5', mRNA sequence.
ACCESSION	60278752F14	EST.
VERSION	BG868714	
KEYWORDS		
ORGANISM	Mus musculus	house mouse.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi;	

REFERENCE
AUTHORS 4 (sites)
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

REFERENCE
AUTHORS 5 (bases 1 to 1199)

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bonoh,H., Brownstein,M., Built,C.,
Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hune,D., Imoriaki,K., Ishii,Y., Iton,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Kurihara,C., Matsumura,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Orido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schrimali,L., Shibata,K., Shiba,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamoto,T., Yamamoto,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 223-0045, Japan; (E-mail: genome-resq@riken.go.jp;
Fax: 81-45-503-9222; Tel: 81-45-503-9222;

COMMENT please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
5', GAGAGAGAGGATCCAAGAGCTTGTGTTTTTTTNTVN 3', cDNA was
prepared by using trehalose thermo activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0 and subtraction to
Rot = 25.0. Second strand cDNA was prepared with the primer adapter
of sequence [5',
GAGAGAGAGTCTGAGTAAATTAATCCCGCCCCCCCC
Host: sour, Cloning sites, 5', end: XbaI, 3', end: SstI.

FEATURES

source 1. 1199

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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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CDS

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DGLAHLKIDFGNEFKNFGTPFVPAETVNEPYLEADWMSIGVYIILS GASPL
GDKOETLANYAVVNDEEBEEFRNISTLAKDFIRLLVQDKKKRMTIOSLQHPIWK
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polyA_signal 1182. .1187

polyA_site 1199

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RESULT 7

LOCUS W82116 869 bp mRNA linear EST 12-SEP-1996

DEFINITION ms98c10_r1 Soares mouse p3MWF19_5 MUS musculus cDNA clone

IMAGE:43602_5 similar to PIR:S39269 S39269 DAP-kinase - human ; mRNA sequence.

ACCESSION W82116

VERSION W82116.1 GI:1393099

Sat May 18 15:09:07 2002

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Search completed: May 17, 2002, 23:36:36
Job time: 5495 sec

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